

FIG. 1

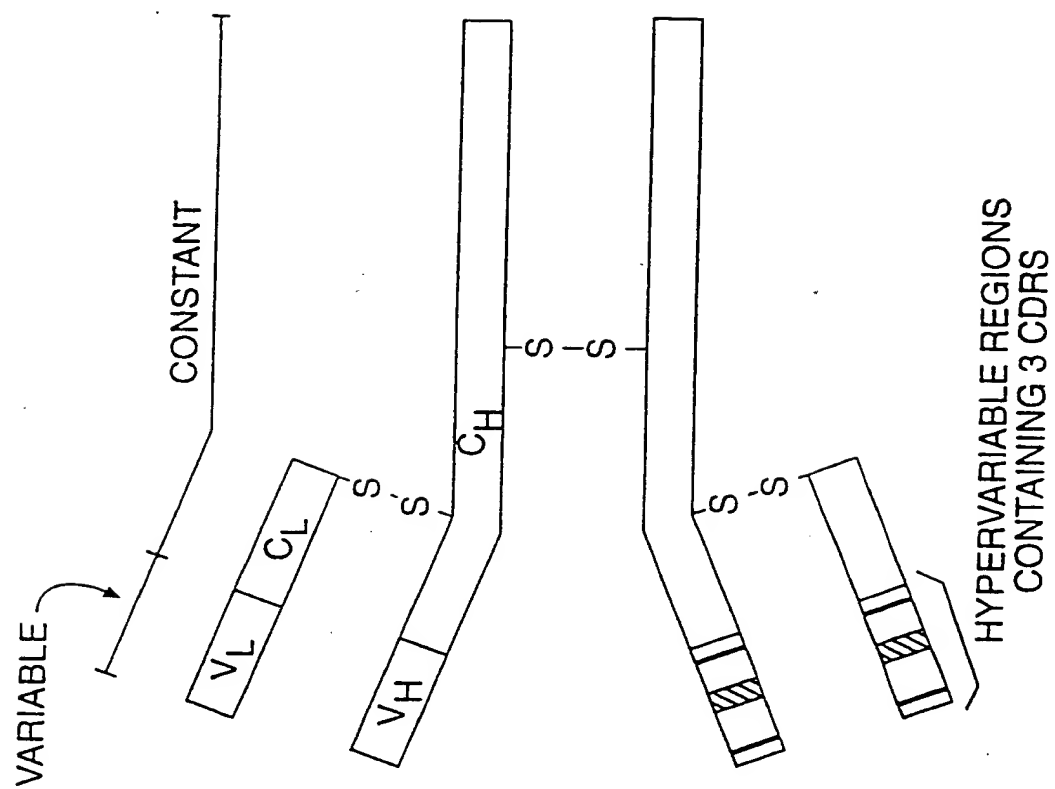


FIG. 2

EFFECT OF ANTI-STAPH MAB 96-110 ON
SURVIVAL IN A LETHAL S.AUREUS SEPSIS MODEL

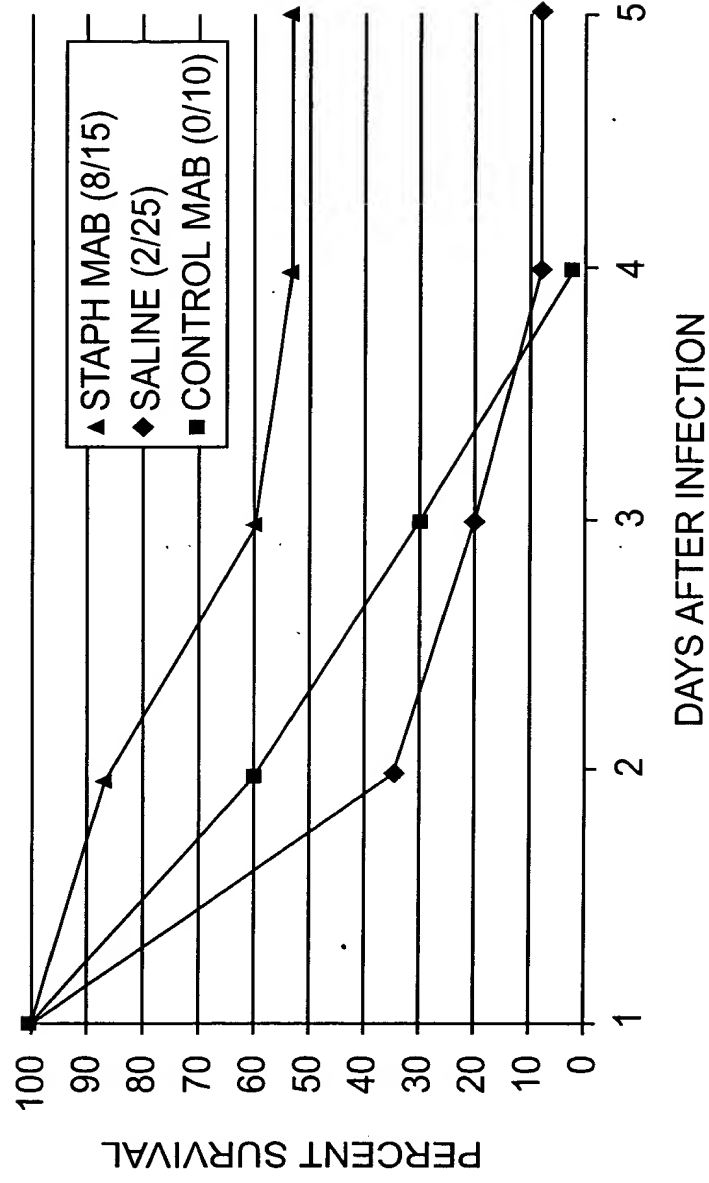


FIG. 3

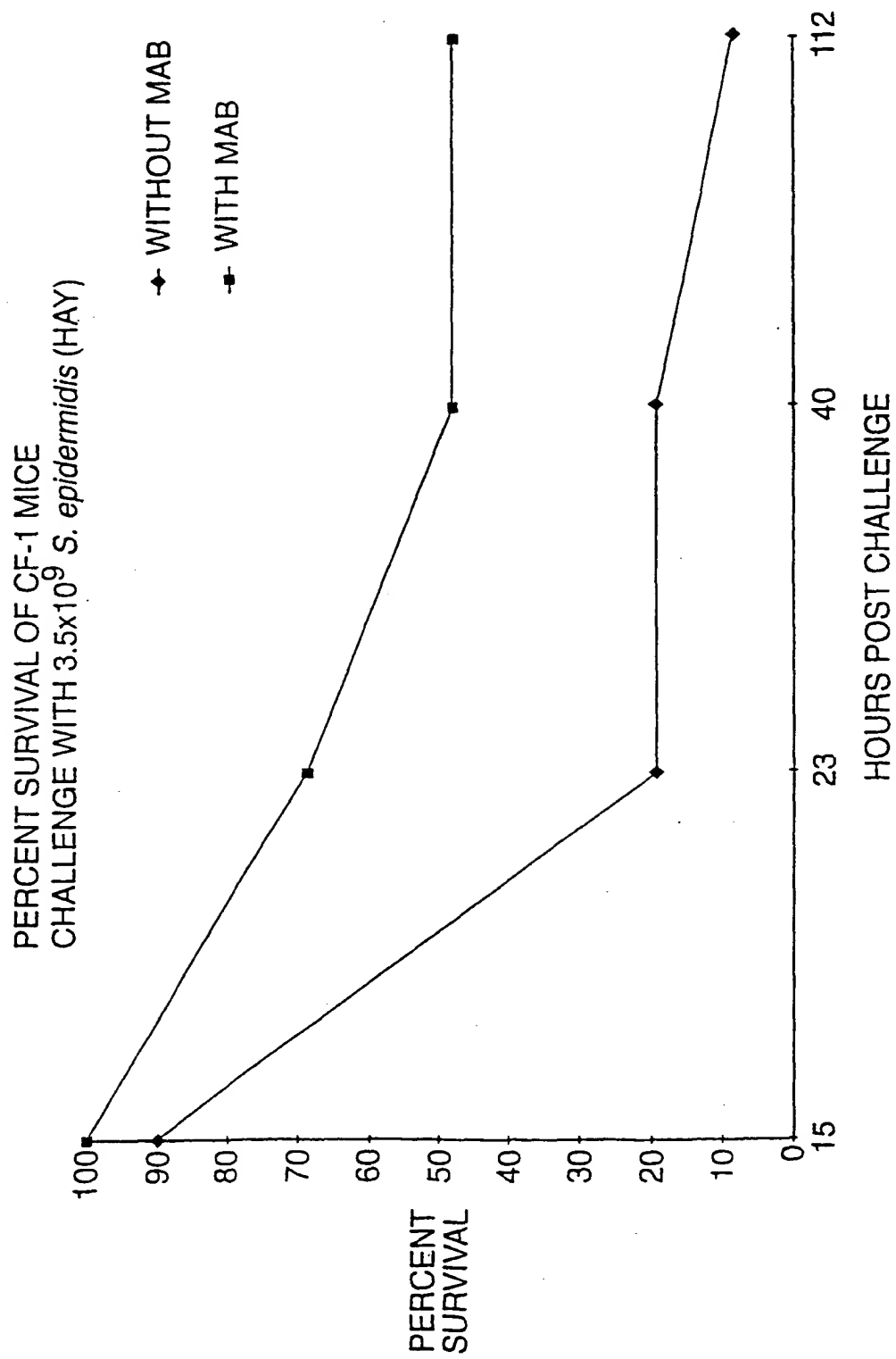


FIG. 4

6MER. SEQ

	10	20	30	
41:13.6mer2-1	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	SEQ ID NO.4
61	C A H	A D R V	Y G A	SEQ ID NO.5
42:14.6mer2-2	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
65	G A H	A D R V	Y G A	
43:15.6mer2-3	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
66	G A H	A D R V	Y G A	
44:16.6mer2-4	GGGA-TCATG	CGGATAGGGT	TTATGGGGCC	SEQ ID NO.6
62	G ? H	A D R V	Y G A	SEQ ID NO.7
45:17.6mer2-5	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
67	G A H	A D R V	Y G A	
46:18.6mer2-6	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
68	G A H	A D R V	Y G A	
47:19.6mer2-7	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
69	G A H	A D R V	Y G A	
48:20.6mer2-8	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
70	G A H	A D R V	Y G A	
49:21.6mer2-9	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
71	G A H	A D R V	Y G A	
51:23.6mer2-11	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
72	G A H	A D R V	Y G A	
52:24.6mer2-12	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
73	G A H	A D R V	Y G A	
53:25.6mer2-13	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
74	G A H	A D R V	Y G A	
54:26.6mer2-14	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
75	G A H	A D R V	Y G A	
55:27.6mer2-15	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
76	G A H	A D R V	Y G A	
56:28.6mer2-16	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
77	G A H	A D R V	Y G A	
58:30.6mer2-18	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
78	G A H	A D R V	Y G A	
59:31.6mer2-19	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
79	G A H	A D R V	Y G A	
60:32.6mer2-20	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
80	G A H	A D R V	Y G A	

FIG. 5

15MER2.SEQ

	10	20	30	40	50	60
50:07.15mer2-1/0	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO.8
70	G A (W)	H W R H	R I P	L Q L A A G R	G A	SEQ ID NO.9
52:09.15mer2-3/0	GGGGCTCGTC	GGGATGGTAA	TTTTTCTCAT	TTTTTTCATC	GGTCGTTTCAT	TGGGGCC SEQ ID NO.10
72	G A R (R)	(H) G N	(F) (S) (H)	F F (H) (R)	S L I G A	SEQ ID NO.11
53:10.15mer2-4/0	GGGGCTTCGA	AGGCTTTGTT	TAGTCATTCT	TATCGTCCTC	GGGGTTCGGC	TGGGGCC SEQ ID NO.12
73	G A (W)	(K) A L (F)	(S) (H) S	Y (R) P R G S A	G A	SEQ ID NO.13
54:11.15mer2-5/0	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO.14
74	G A R H W R H	R I P	L Q L A A G R	G A	SEQ ID NO.15	
56:13.15mer2-7/0	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO.16
76	G A W H W R H	R I P	L Q L A A G R	G A	SEQ ID NO.17	
57:14.15mer2-8/0	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO.18
77	G A W H W R H	R I P	L Q L A A G R	G A	SEQ ID NO.19	
58:15.15mer2-9/0	GGGGCTCAGG	TGGCTGTTTT	CTATCCTCCT	TTGGCTGATG	CTACTGAGCT	TGGGGCC SEQ ID NO.20
78	G A Q V A V L	Y P P	L A D A T E L	G A	SEQ ID NO.21	
59:16.15mer2-10/0	GGGGCTCGTC	GGGATGGTAA	TTTTTCTCAT	TTTTTTCATC	GGTCGTTTCAT	TGGGGCC SEQ ID NO.22
79	G A R R H G N	F S H	F F H R S L I	G A	SEQ ID NO.23	
60:17.15mer2-11/0	GGGGCTCGTC	GGGATGGTAA	TTTTTCTCAT	TTTTTTCATC	GGTCGTTTCAT	TGGGGCC SEQ ID NO.24
80	G A R R H G N	F S H	F F H R S L I	G A	SEQ ID NO.25	
61:18.15mer2-12/0	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATGGGCATC	TTCGTAAGTCC	TGGGGCC SEQ ID NO.26
81	G A (W)	R M Y (F)	(S) (H) R	H A (H) (L)	R S P G A	SEQ ID NO.27
62:19.15mer2-13/0	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATGGGCATC	TTCGTAAGTCC	TGGGGCC SEQ ID NO.28
82	G A W R M Y F	S H R	H A H L R S P	G A	SEQ ID NO.29	
63:20.15mer2-14/0	GGGGCTTGGC	GGAAGTATTT	TTCTTATCAT	CATGGGCATC	TTTGTAAGTCC	TGGGGCC SEQ ID NO.30
83	G A W R M Y F	S Y H	H A H L C S P	G A	SEQ ID NO.31	
64:21.15mer2-15/0	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATGGGCATC	TTCGTAAGTCC	TGGGGCC SEQ ID NO.32
84	G A W R M Y F	S H R	H A H L R S P	G A	SEQ ID NO.33	
65:22.15mer2-16/0	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATGGGCATC	TTCGTAAGTCC	TGGGGCC SEQ ID NO.34
85	G A W R M Y F	S H R	H A H L R S P	G A	SEQ ID NO.35	

FIG. 6A

15MER2.SEQ		10	20	30	40	50	60
66:23.15mer2-17/0	86	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATGGCATC	TTCGTAGTCC	TGGGGCC SEQ ID NO.36
		G A W	R M Y F	S H R	H A H	L R S P	G A SEQ ID NO.37
67:24.15mer2-18/0	87	GGGGCTCGTC	GGCATGGTAA	TTTTTCTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO.38
		G A H	R H G N	F S H	F F H	R S L I	G A SEQ ID NO.39
68:25.15mer2-19/0	88	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO.40
		C A W	H W R H	R I P	L Q L	A A G R	G A SEQ ID NO.41
69:26.15mer2-20/0	89	GGGGCTCGTC	GGCATGGTAA	TTTTTCTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO.42
		G A H	R H G N	F S H	F F H	R S L I	G A SEQ ID NO.43

FIG. 6B

15MER1.SEQ

	10	20	30	40	50	60
51:28.15mer1-2/0	GGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC SEQ ID NO.44
67	G A D (W) I T (F) (H) R R	H (H) D (R) V L S	G A	SEQ ID NO.45		
52:29.15mer1-3/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC SEQ ID NO.46
68	G A D W I T F H R R	H R R H H D	R V L S	G A	SEQ ID NO.47	
53:32.15mer1-6/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
65	G A D W I T F H R R	H R R H H D	R V L S	G A		
62:13.15mer1-7/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
66	G A D W I T F H R R	H R R H H D	R V L S	G A		
63:14.15mer1-8/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
67	G A D W I T F H R R	H R R H H D	R V L S	G A		
64:15.15mer1-9/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
68	G A D W I T F H R R	H R R H H D	R V L S	G A		
65:16.15mer1-10/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
69	G A D W I T F H R R	H R R H H D	R V L S	G A		
56:17.15mer1-11/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
70	G A D W I T F H R R	H R R H H D	R V L S	G A		
57:28.15mer1-12/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
71	G A D W I T F H R R	H R R H H D	R V L S	G A		
58:29.15mer1-13/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
72	G A D W I T F H R R	H R R H H D	R V L S	G A		
59:20.15mer1-14/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
73	G A D W I T F H R R	H R R H H D	R V L S	G A		
70:21.15mer1-15/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
74	G A D W I T F H R R	H R R H H D	R V L S	G A		
71:22.15mer1-16/0	GGGGCTGGGA	AGGCTATGTT	TATCGTATCT	TATCGTATCT	GGGGTTCGGC	TGGGGCC SEQ ID NO.48
75	G A D (K) A M (F) (S) (H) S Y R (H) (R) G S A	G A	SEQ ID NO.49			
72:23.15mer1-17/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
76	G A D W I T F H R R	H R R H H D	R V L S	G A		

FIG. 7A

15MER1.SEQ

	10	20	30	40	50	60
73:24.15mer1-18/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
77	G A D W I T F	H R R H H D	R V L S G A			
74:25.15mer1-19/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
78	G A D W I T F	H R R H H D	R V L S G A			
75:26.15mer1-20/0	GGGGCTGGTT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC
79	G A D W I T F	H R R H H D	R V L S G A			

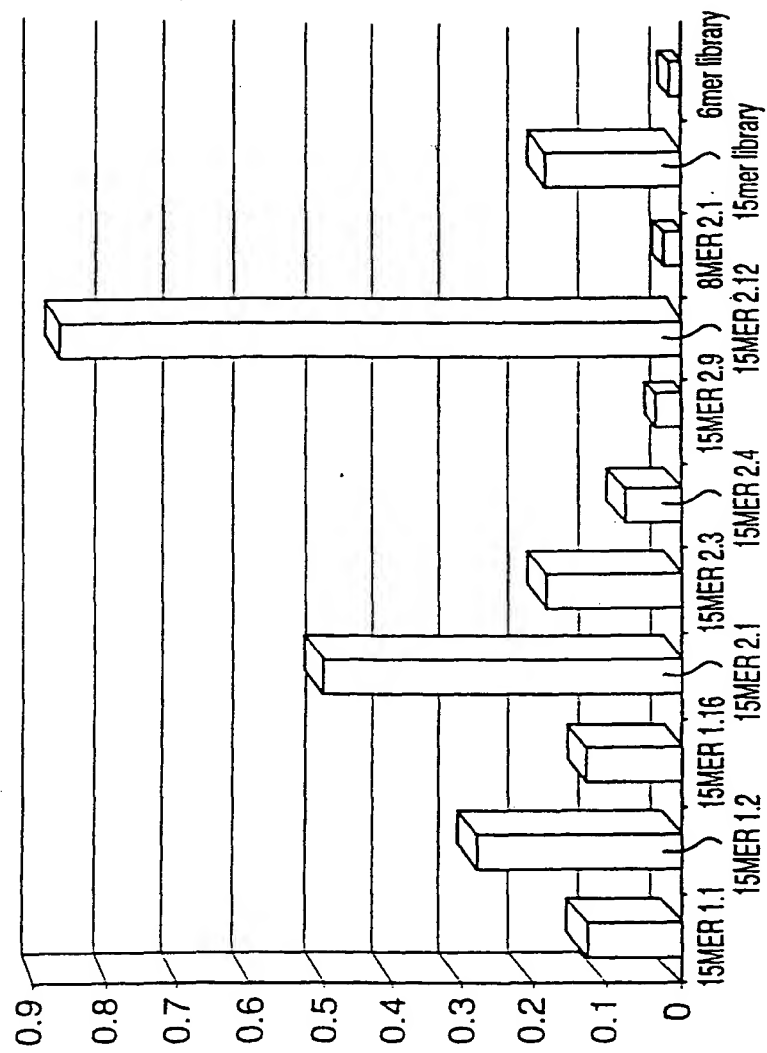
FIG. 7B

masterlist

	10	20	30	40	50	60	70
51:15mer 1st.1	GGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	16/17 SEQ ID NO.50
57	G A D	W I T F	H R R	H H D	R V L S	G A	SEQ ID NO.51
90 15mer 1st.2	GGGGCTAGTC	GTCATATGCT	TGCTCGGTGG	TCGCGTTTGC	TTGCTGTTTC	TGGGGCC	1/10 SEQ ID NO.52
91	G A S	R H M L	A R W	S R L	L A V P	G A	SEQ ID NO.53
71:15mer 1st.16	GGGGCTGGGA	AGGCTATGTT	TAGTCATTCT	TATCGTCATC	GGCGTTCGGC	TGGGGCC	1/17 SEQ ID NO.54
85	G A G	K A M F	S H S	Y R H	R G S A	G A	SEQ ID NO.55
92 15mer 2nd.1	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC	5/18 SEQ ID NO.56
98	G A W	H W R H	R I P	L Q L	A A G R	G A	SEQ ID NO.57
93 15mer 2nd.3	GGGGCTCGTC	GGCATGGTAA	TTTTTCTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC	6/18 SEQ ID NO.58
99	G A R	R H G N	F S H	F F H	R S L I	G A	SEQ ID NO.59
94 15mer 2nd.4	GGGGCTTGGGA	AGGCTTTGTT	TAGTCATTCT	TATCGTCCTC	GGGGTTCGGC	TGGGGCC	1/18 SEQ ID NO.60
100	G A W	X A L F	S H S	Y R P	R G S A	G A	SEQ ID NO.61
95 15mer 2nd.9	GGGGCTCAGG	TGGCTGTTTT	GTATCCTCCT	TTGGCTGATG	CTACTGAGCT	TGGGGCC	1/18 SEQ ID NO.62
101	G A Q	V A V L	Y P P	L A D	A T E L	G A	SEQ ID NO.63
96 15mer 2nd.12	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATCGGCATC	TTCGTAGTCC	TGGGGCC	6/18 SEQ ID NO.64
102	G A W	R M Y F	S H R	H A H	L R S P	G A	SEQ ID NO.65
97 6mer 2nd.1	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC				18/18 SEQ ID NO.66
103	G A H	A D R V	Y G A				SEQ ID NO.67

FIG. 8

COMPARISON OF SIGNALS AT 6.25x10⁸ virus/mL



3RD ROUND ISOLATES

FIG. 9

GENERAL CLONING STRATEGY

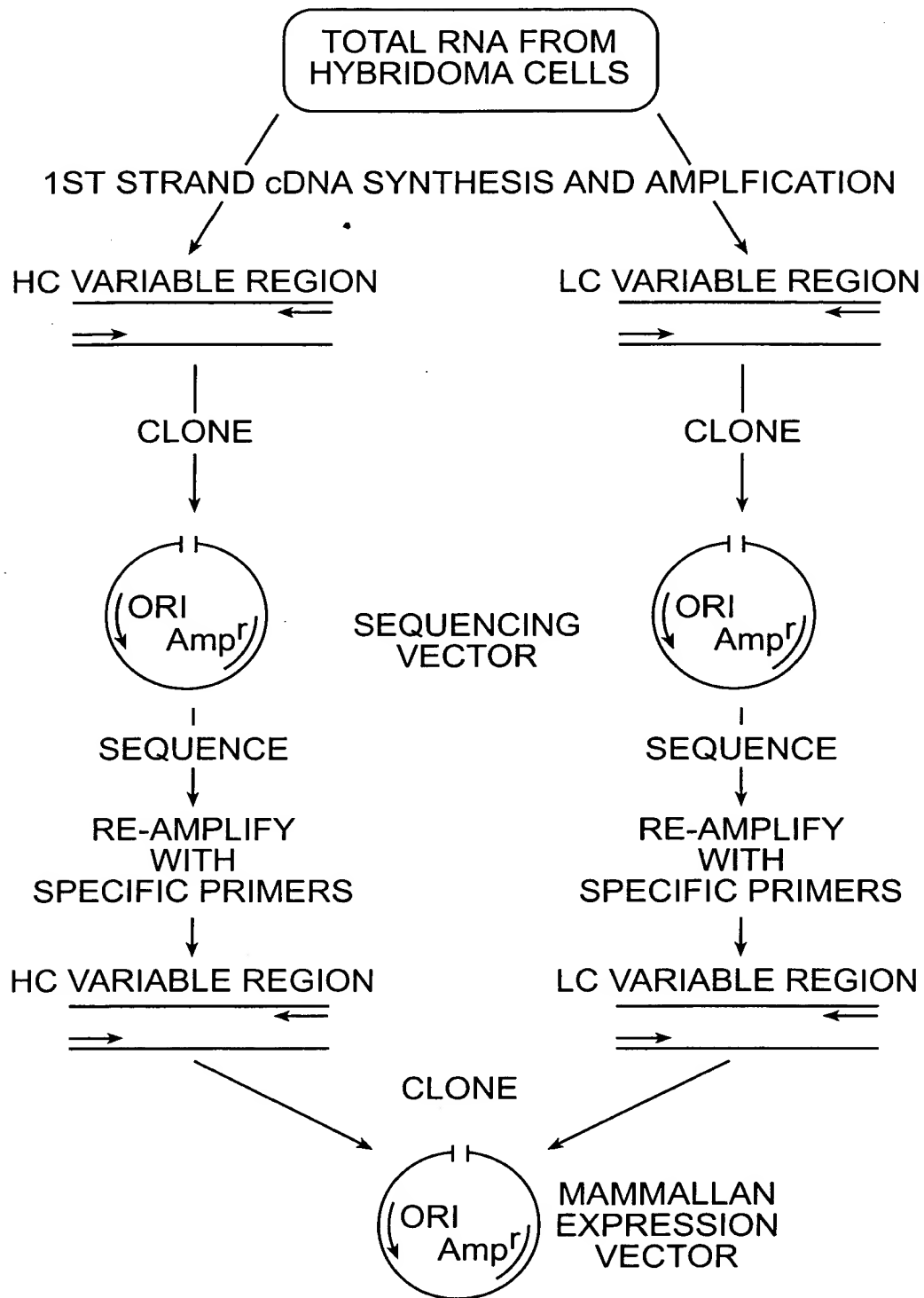


FIG. 10

MOUSE HEAVY CHAIN "FRONT" PRIMERS

JSS1

5' -ATTTCAGGCCCGGCCCATGGCCGARGTRMAGCTKSAKGAGWC-3' SEQ ID NO. 68

JSS2

5' -ATTTCAGGCCCGGCCCATGGCCGARGTYCARCTKCARCARYC-3' SEQ ID NO. 69

JSS3

5' -ATTTCAGGCCCGGCCCATGGCCCGAGGTGAAGCTKSTSGARTC-3' SEQ ID NO. 70

JSS4

5' -ATTTCAGGCCCGGCCCATGGCCGAVGTGMWGCCTKGTGGAGWC-3' SEQ ID NO. 71

JSS8

5' -ATTTCAGGCCCGGCCCATGGCCCGAGGTBCARCTKMARSARTC-3' SEQ ID NO. 72

MOUSE HEAVY CHAIN "BACK" PRIMERS

JS160

5' -GCTGCCACCGCCACCTGMRGAGACDGTGASTGARG-3' SEQ ID NO. 73

JS161

5' -GCTGCCACCGCCACCTGMRGAGACDGTGASMGTRG-3' SEQ ID NO. 74

JS162

5' -GCTGCCACCGCCACCTGMRGAGACDGTGASCARG-3' SEQ ID NO. 75

FIG. 11A

MOUSE LIGHT CHAIN LEADER "FRONT" PRIMERS

PMC12

5'-CCCCGGCCACCATGGAGACAGACACTCCTG-3' SEQ ID NO.76

PMC13

5'-CCCCGGCCACCATGGATTTTCAAGTGCAGATTTTC-3' SEQ ID NO.77

PMC14

5'-CCCCGGCCACCATGGAGWCACAKWCTCAGGTC-3' SEQ ID NO.78

PMC15

5'-CCCCGGCCACCATGKCCCCWRCTCAGYTTCTKG-3' SEQ ID NO.79

PMC55

5'-CCCCGGCACCATGAAGTTGCCCTGTAGGCTG-3' SEQ ID NO.80

MOUSE LIGHT CHAIN "BACK" PRIMER

OKA57

5'-GCACCTCCAGATGTTAACTGCTC-3' SEQ ID NO. 81

"96-110" SPECIFIC PRIMERS

96110HF2

5'-TAATATCGGCACAGCTACAGGTGTCCACTCCCGAAGTGATGCTGGTGGAGWCTG-3' SEQ ID NO.82

96100HB

5'-TTATAGAATTCTGAGGAGACGGTGAGTGAG-3' SEQ ID NO.83

96110BLF

5'-TTAGGCGATAGCGTTCTCTCCAGTCTCC-3' SEQ ID NO.84

96110BLB

5'-GTAACCG TTCGAAAAGTGACTTACGTTTATTTCACGATGGTCC-3' SEQ ID NO.85

FIG. 11B

96-110 ANTI-STAPH (HAY) HEAVY CHAIN VARIABLE REGION (TYPE IIIA)

GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTACCTTCAAT
E V M L V E S G G G L V Q P K G S L K L S C A A S G F T F N

AACTACGCCATGAAT TGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAAATGGGTGCT
N Y A M N W V R Q A P G K G L E W V A

CGCATAAGTAAGTAAATAATTATGCAACATTTTATGCCGATTTCAGTGAAAGAC
R I R S K S N N Y A T F Y A D S V K D

AGTTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCTGCAAAATGAACAACCTTGAAAACCTGAGGACACAGCCATGTATTACTGTGTGAGA
R F T I S R D D S Q S M L Y L Q M N N L K T E D T A M Y Y C V R

CGGGGGCTTCAGGGATTGACTATGCTATGGACTAC TGGGGTCAAGGAACCTCACTCACCGTCTCCTCA SEQ ID NO. 86
R G A S G I D Y A M D Y W G Q G T S L T V S S SEQ ID NO. 87

FIG. 12A

96-110 ANTI-STAPH (HAY) LIGHT CHAIN VARIABLE REGION (TYPE VI)

CAAATTGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACAATGACTTGC
Q I V L S Q S P A I L S A S P G E K V T M T C

AGGCCAGCTCAAGTGTAATTACATGCAC
R A S S S V N Y M H

TGGTACCAGCAGAAGCCAGGATCCTCCCCAAACCCTGGATTCT GCCACATCCAACCTGGCTTCT
W Y Q Q K P G S S P K P W I S A T S N L A S

GGAGTCCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGC
G V P A R F S G S G S G T S Y S L T I S R V E A E D A A T Y Y C

CAGCAGTGGAGTAGTAACCCACCACG TTCGAGGGGGGACCATGCTGGAAATAAGA SEQ ID NO. 88
Q Q W S S N P P T P G G G T M L E I R SEQ ID NO. 89

CDR REGIONS UNDERLINED

FIG. 12B

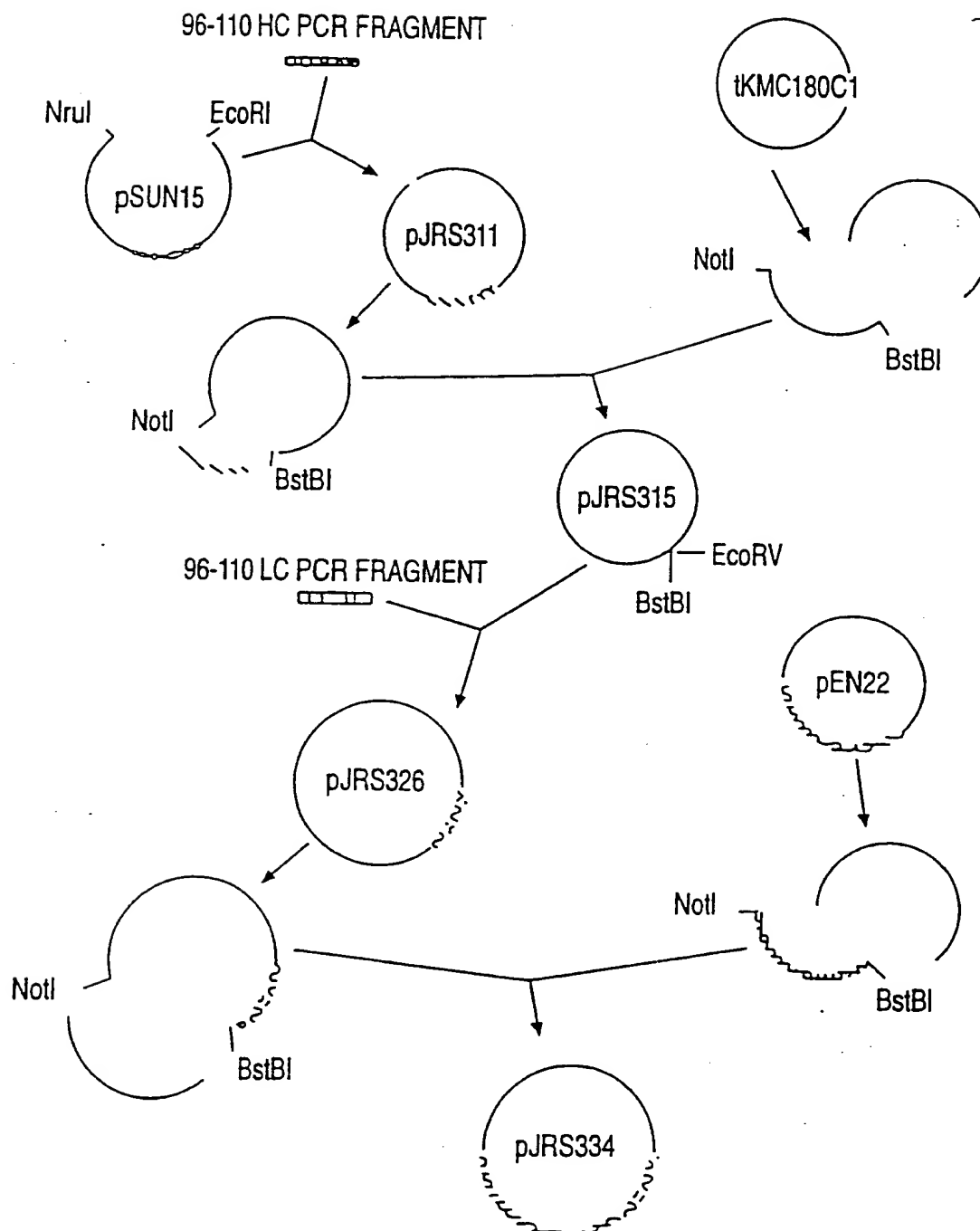
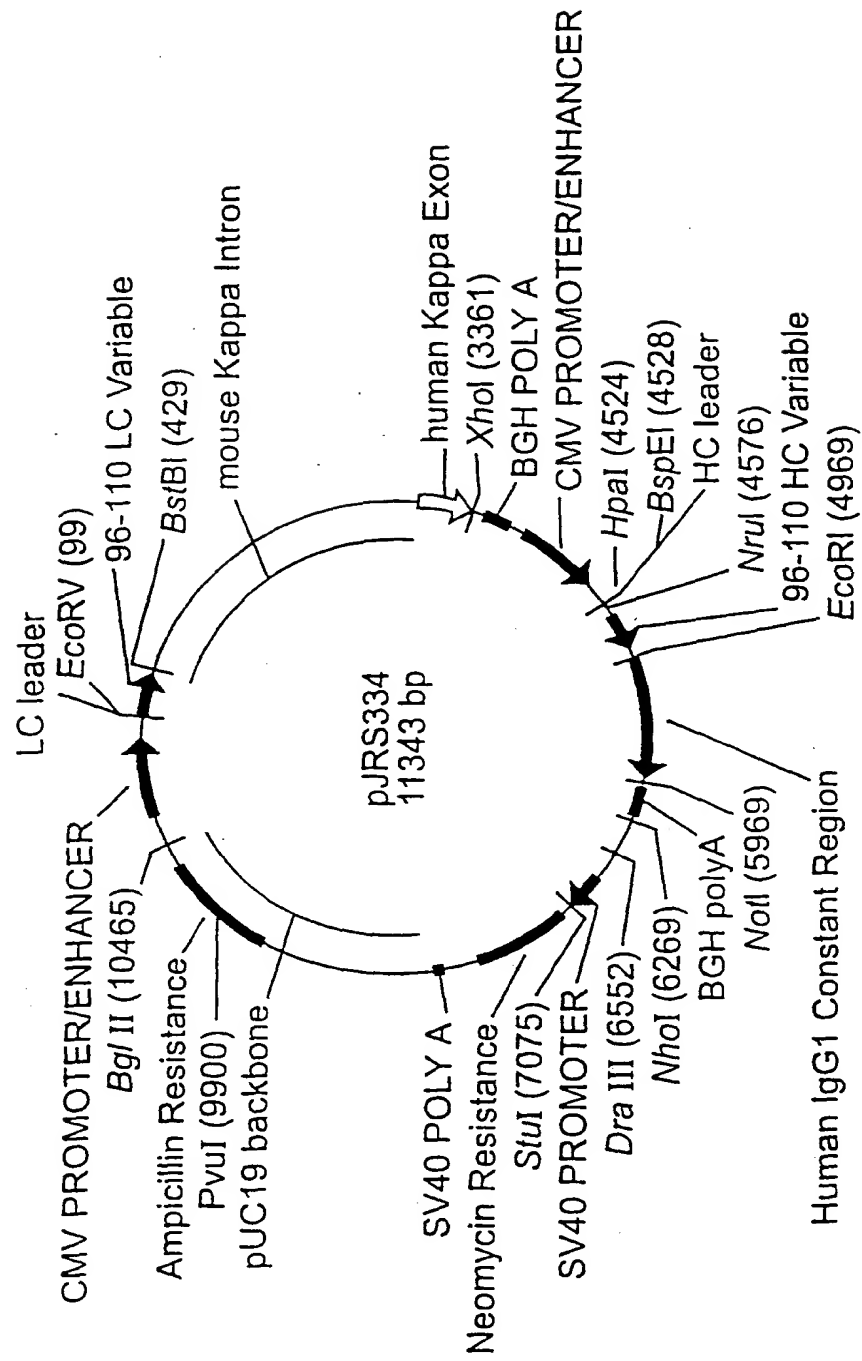


FIG. 13



Common Unique Restriction Sites Shown

FIG. 14

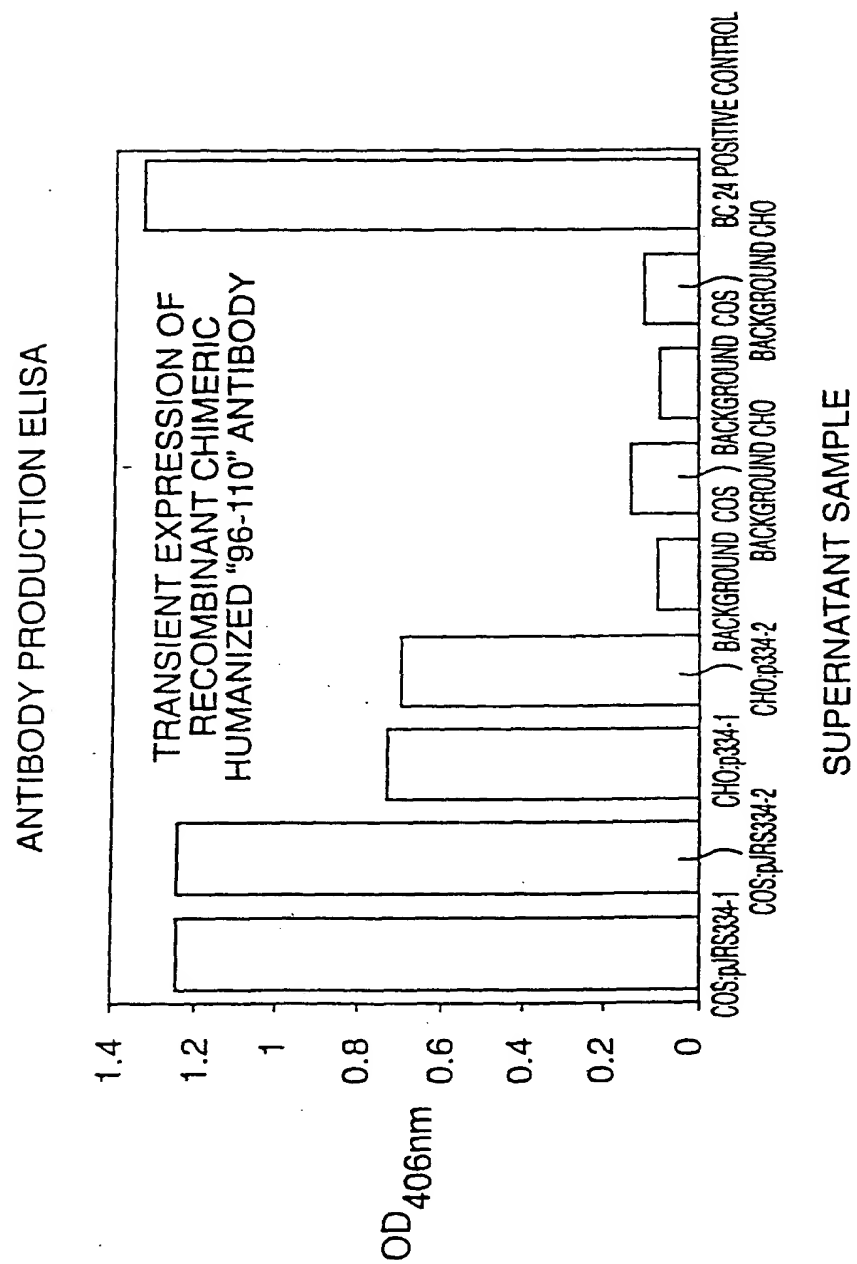


FIG. 15

ANTI-STAPH HAY ACTIVITY ELISA

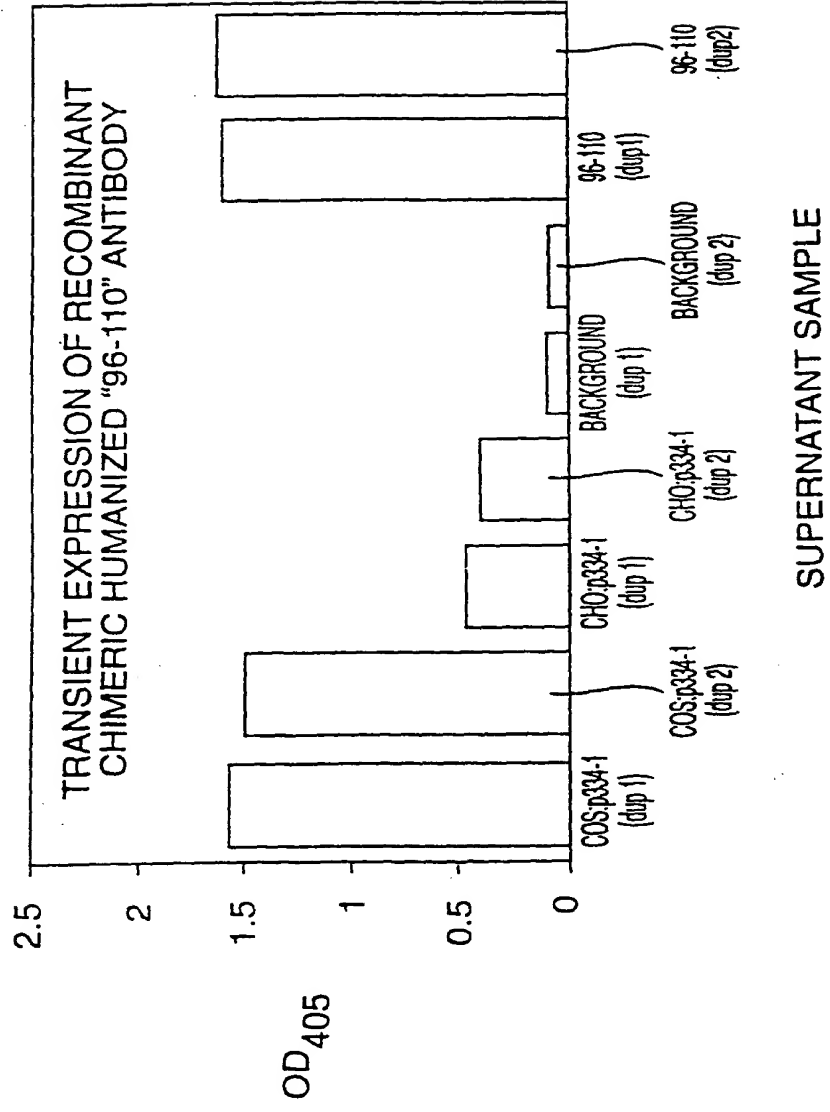
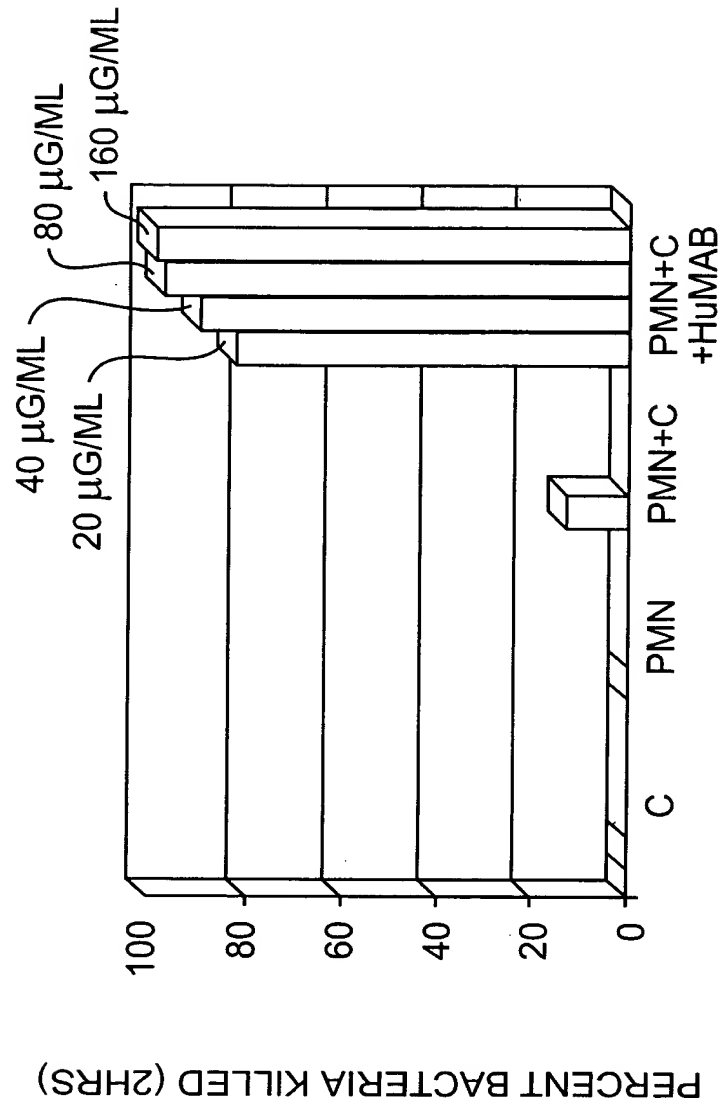


FIG. 16

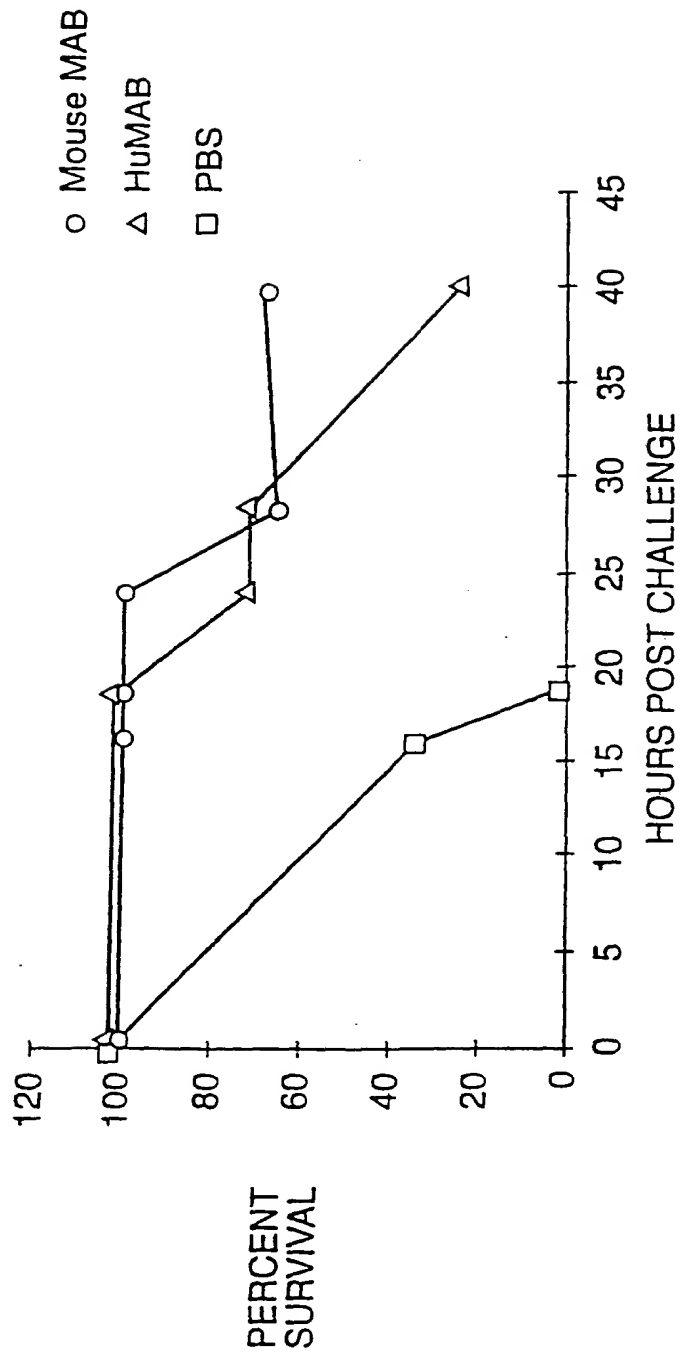
OPSONIC ACTIVITY OF HuMAB 96-110 FOR S.EPIDERMIDIS
 IN A NEUTROPHIL MEDIATED OPSONOPHAGOCYTIC
 BACTERICIDAL ASSAY USING HUMAN COMPLEMENT



C- BACK-EX (1:D), HUMAN
 PMN-HUMAN
 BACTERIA-S.EPIDERMIDIS (STRAIN HAY)

FIG. 17

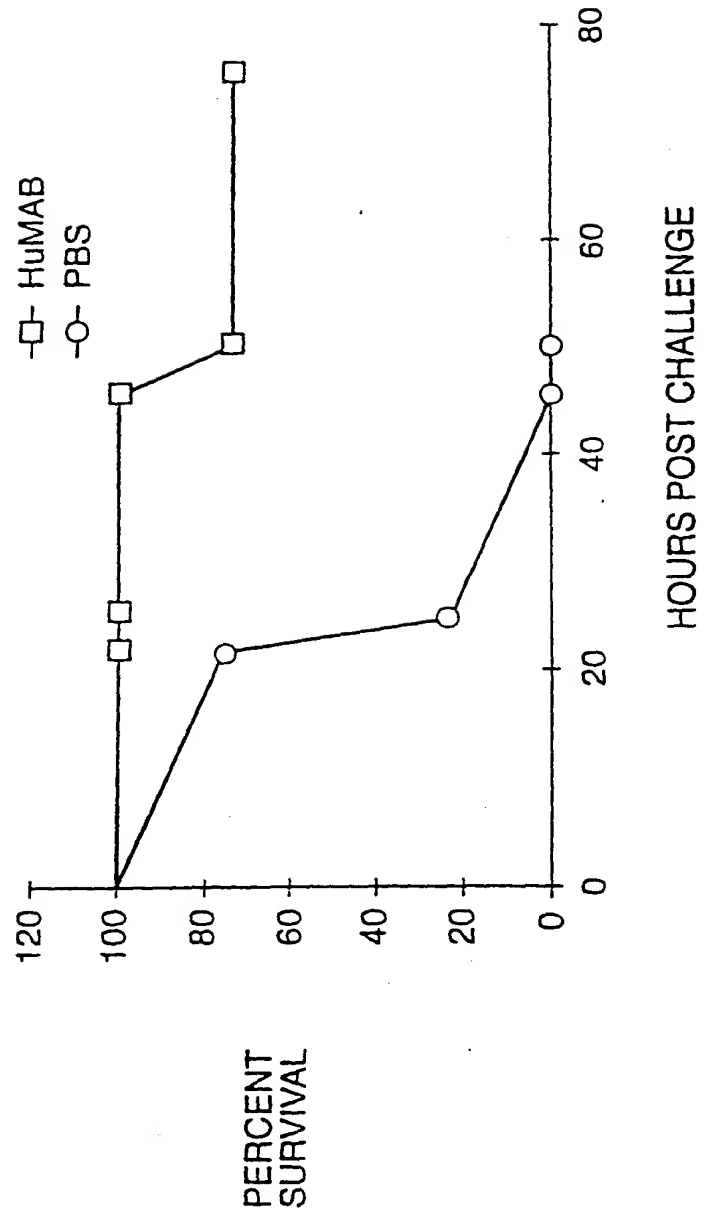
Pilot Study to Compare the Effect of Mouse
MAB 96-110 and HuMAB 96-110 in a Lethal
Model of *S. epidermidis* Sepsis



MAB dose: 14 mg/kg given IP, 24 and 1 hour prior to infection

FIG. 18

Survival of CF-1 Mice after Intraperitoneal
Challenge with 3×10^9 *S. epidermidis* (HAY)



18 mg/kg/dose, IP, 24 and 1 hour prior to infection

FIG. 19

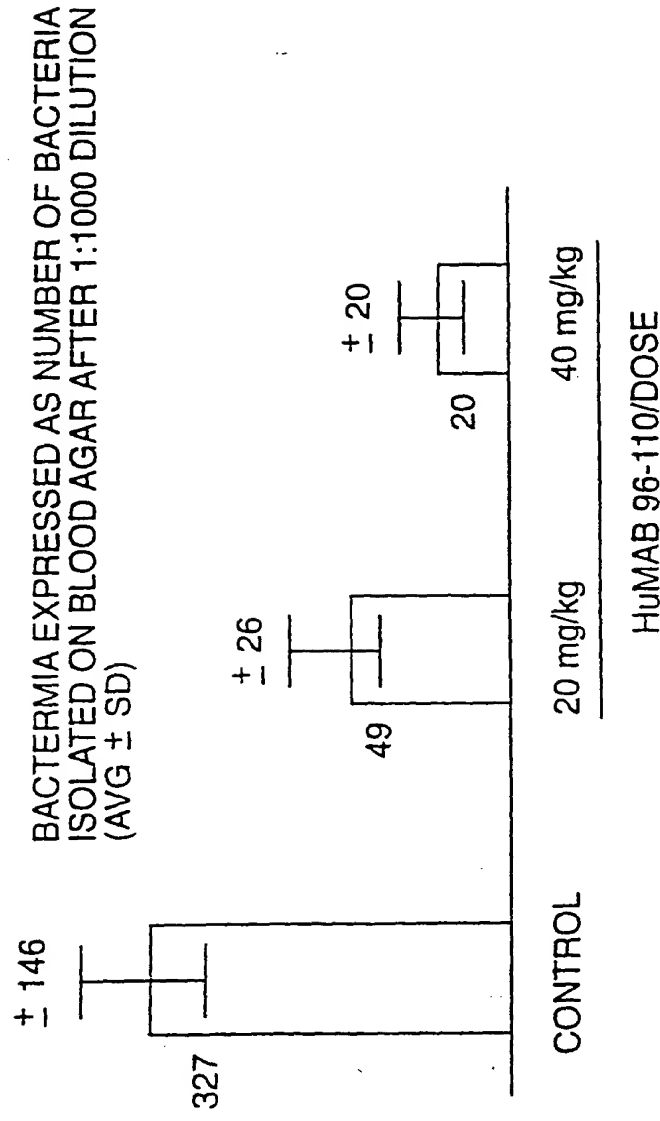
Effect of HuMAB 96-110 on Bacteremia in a Lethal *S. epidermidis* Sepsis Model

Geometric Mean Bacteremia Level				
Saline Placebo	6.5 x 10 ⁴	7.2 x 10 ⁴	5.2 x 10 ⁴	7 x 10 ³
HuMAB 96-110	3 x 10 ²	7.5 x 10 ²	2.1 x 10 ¹	1.7 x 10 ¹
	4 hrs	8 hrs	12 hrs	18 hrs

HuMAB 96-110 18 mg/kg/dose or saline given IP, 24 and 1 hour
prior to IP infection with 3x10⁹ *S. epidermidis* (Hay)

FIG. 20

BACTEREMIA LEVELS 4 HRS AFTER INFECTION WITH 3×10^9 S. EPIDERMIDIS*

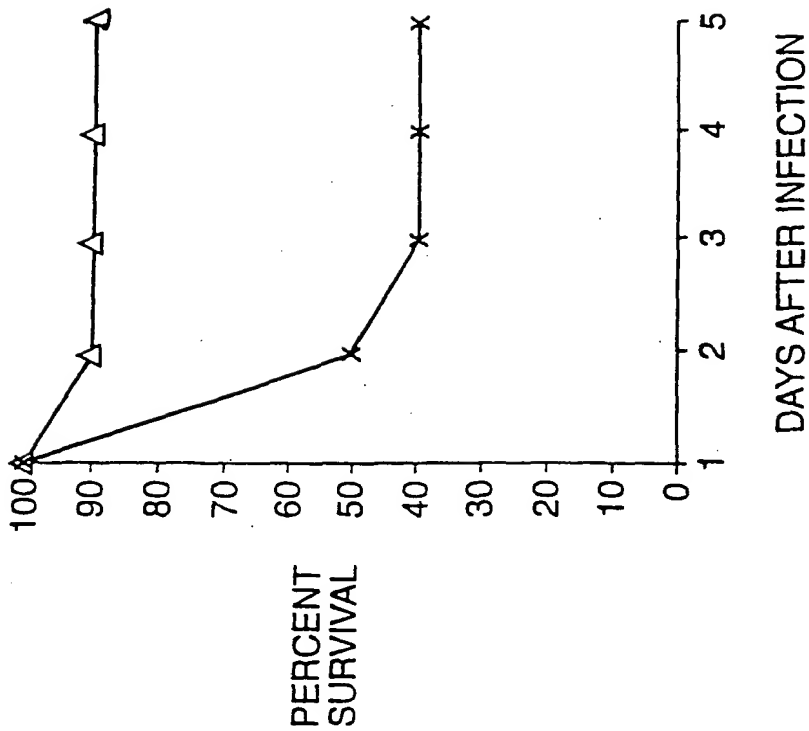


*CF-1 MICE INFECTED IP WITH STRAIN HAY-HuMAB GIVEN IPx2

FIG. 21

The Effect of Hu 96-110 on Survival in a
Lethal Neonatal *S. epidermidis* * Sepsis Model

SURVIVAL:
HU 96-110 27/30 (90%)
SALINE 12/30 (40%)



-△- HuMAB 96-110
-x- SALINE CONTROL
* 4 DIFFERENT SE STRAINS

STUDY II:
INFECTION-- 5×10^7 SE, SQ (WITH PLASTIC CATHETER SQ)
LIPID EMULSION-0.2ml, 20% IP DAY-1 AND +1,2 DOSES DAY 0
HuMAB OR SALINE-0.2ml, IP 30 MIN BEFORE AND 24 HRS
AFTER INFECTION
DOSE: 50-60 mg/kg PER DOSE

FIG. 22